



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/706,435
Source: JFWO
Date Processed by STIC: 2/1/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/706,435</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING

DATE: 07/01/2004

PATENT APPLICATION: US/10/706,435

TIME: 13:19:35

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\07012004\J706435.raw

2 <110> APPLICANT: Walter Reed Army Institute of Research
 3 Lanar, David E.
 4 Hillier, Collette J.
 5 Lyon, Jeffrey A.
 6 Angov, Evelina
 7 Kumar, Sanjai
 8 Rogers, William
 9 Barbosa, Arnoldo
 11 <120> TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
 12 falciparum Liver Stage Antigen 1 Polypeptide
 14 <130> FILE REFERENCE: 003/285/SAP
 16 <140> CURRENT APPLICATION NUMBER: 10/706,435
 18 <141> CURRENT FILING DATE: 2003-11-12
 20 <150> PRIOR APPLICATION NUMBER: 60/425,719
 22 <151> PRIOR FILING DATE: 2002-11-12
 E--> 24 <160> NUMBER OF SEQ ID NOS: (28) 27 (p.2)
 26 <170> SOFTWARE: Microsoft Word XP

ERRORED SEQUENCES

201 <210> SEQ ID NO: 5
 202 <211> LENGTH: 17
 203 <212> TYPE: PRT
 204 <213> ORGANISM: Artificial sequence
 W--> 205 <220> FEATURE:
 Xaa at location 4
 206 <223> OTHER INFORMATION: Consensus sequence of 17 amino acid repeats where (x1)
 207 is either Glu or Gly; (x2) is Ser or Arg; (x3) is Asp or Ser; (x4)
 208 is Glu or Asp; (x5) is Leu or Arg; (x6) is Lys or Asn and (x7) is
 209 Lys or Thr or Arg.
 W--> 210 <400> SEQUENCE: 5
 E--> 211 (X1) Gln Gln (X2) Asp (X3) Glu Gln (X4) Arg
 E--> 212 5
 E--> 214 (X5) Ala (X6) Glu (X7) Leu Gln
 E--> 215 5-15-15, not 5
 E--> 372 <210> SEQ ID NO: 19

Does Not Comply
 Corrected Diskette Needed

(Seq 18 is missing)

see p.2

Xaa at location 1

Do NOT represent Xaa as X₁, X₂, etc.
 Use Xaa only, and use <222>
 to show locations of Xaa's.
 E.g. <222> 1,4,6,9,11,13,15

misaligned amino acid numbers.
 See item 3 on Error Summary
 sheet.

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2

<400> 17

His Thr Leu Glu Thr Val Asn Ile Ser Asp
5 10

Val Asn Asp Phe Gln Ile Ser Lys Tyr Glu
15 20

Asp Glu Asp Leu Asp Glu Phe Lys Pro Ile
25 30

Val Gln Tyr Asp Asn Phe Gln Asp
35

<210> 19

→ Sequence 18 missing
(see p.3)

RAW SEQUENCE LISTING ERROR SUMMARY
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IMPORTANT

Skipped Sequences (NEW RULES):

Sequence(s) __missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

000

Seq#:18

see p. 4 for more errors

<210> 3
 <211> 1374
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> isa-nrc^{Hmut}
 <400> 3

do not use italics or raised text or bold print

Per 1.823 of Sequence Rules: "a

fixed-width
font should be
used exclusively
throughout the
'Sequence Listing.'"

also,
when explaining
"Artificial Sequence",
please give source
of genetic material on
<223> line

The above is a sample of these
types of errors throughout the Sequence
Listing.

VERIFICATION SUMMARY

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Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\07012004\J706435.raw

L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:34 M:283 W: Missing Blank Line separator, <400> field identifier
L:45 M:283 W: Missing Blank Line separator, <220> field identifier
L:47 M:283 W: Missing Blank Line separator, <400> field identifier
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:283 W: Missing Blank Line separator, <400> field identifier
L:103 M:283 W: Missing Blank Line separator, <220> field identifier
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:205 M:283 W: Missing Blank Line separator, <220> field identifier
L:210 M:283 W: Missing Blank Line separator, <400> field identifier
L:211 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:211 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:4
L:212 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:214 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:214 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:3
L:215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:221 M:283 W: Missing Blank Line separator, <220> field identifier
L:223 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:283 W: Missing Blank Line separator, <220> field identifier
L:236 M:283 W: Missing Blank Line separator, <400> field identifier
L:246 M:283 W: Missing Blank Line separator, <220> field identifier
L:248 M:283 W: Missing Blank Line separator, <400> field identifier
L:258 M:283 W: Missing Blank Line separator, <220> field identifier
L:260 M:283 W: Missing Blank Line separator, <400> field identifier
L:272 M:283 W: Missing Blank Line separator, <220> field identifier
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:287 M:283 W: Missing Blank Line separator, <220> field identifier
L:289 M:283 W: Missing Blank Line separator, <400> field identifier
L:297 M:283 W: Missing Blank Line separator, <220> field identifier
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:310 M:283 W: Missing Blank Line separator, <220> field identifier
L:312 M:283 W: Missing Blank Line separator, <400> field identifier
L:320 M:283 W: Missing Blank Line separator, <220> field identifier
L:322 M:283 W: Missing Blank Line separator, <400> field identifier
L:334 M:283 W: Missing Blank Line separator, <220> field identifier
L:336 M:283 W: Missing Blank Line separator, <400> field identifier
L:347 M:283 W: Missing Blank Line separator, <220> field identifier
L:349 M:283 W: Missing Blank Line separator, <400> field identifier
L:360 M:283 W: Missing Blank Line separator, <220> field identifier
L:362 M:283 W: Missing Blank Line separator, <400> field identifier
L:372 M:214 E: (33) Seq.# missing, SEQ ID NO:18
L:376 M:283 W: Missing Blank Line separator, <220> field identifier
L:378 M:283 W: Missing Blank Line separator, <400> field identifier
L:387 M:283 W: Missing Blank Line separator, <220> field identifier
L:389 M:283 W: Missing Blank Line separator, <400> field identifier
L:400 M:283 W: Missing Blank Line separator, <220> field identifier
L:402 M:283 W: Missing Blank Line separator, <400> field identifier
L:412 M:283 W: Missing Blank Line separator, <220> field identifier

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L:414 M:283 W: Missing Blank Line separator, <400> field identifier
L:425 M:283 W: Missing Blank Line separator, <220> field identifier
L:427 M:283 W: Missing Blank Line separator, <400> field identifier
L:435 M:283 W: Missing Blank Line separator, <220> field identifier
L:438 M:283 W: Missing Blank Line separator, <400> field identifier
L:451 M:283 W: Missing Blank Line separator, <220> field identifier
L:453 M:283 W: Missing Blank Line separator, <400> field identifier
L:495 M:283 W: Missing Blank Line separator, <220> field identifier
L:497 M:283 W: Missing Blank Line separator, <400> field identifier
L:598 M:283 W: Missing Blank Line separator, <220> field identifier
L:600 M:283 W: Missing Blank Line separator, <400> field identifier
L:608 M:283 W: Missing Blank Line separator, <220> field identifier
L:610 M:283 W: Missing Blank Line separator, <400> field identifier
L:24 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (28) Counted (27)